

BLASTX ALIGNMENT OF SEQ ID NO: 4, CADHERIN-LIKE POLYPEPTIDE WITH HUMAN OB-CADHERIN-1 POLYPEPTIDE SEQ ID NO: 16

Query: Cadherin-like polypeptide (SEQ ID NO: 4)
 Subjct: dbj|BAA04798.1| (D21254) OB-cadherin-1 [Homo sapiens] (SEQ ID NO: 16)
 Length = 796

Score = 1478 (525.3 bits), Expect = 2.1e-164, Sum P(2) = 2.1e-164
 Identities = 269/419 (64%), Positives = 341/419 (81%), Frame = +1

Query: 283 GPALLRTRRSWVNQFFVIEEYAGPEPVLIGKLHSDVDRGGRTKYLLTGEGAGTVFVID 462
 G L R++R WVNQFFVIEEY GP+PVL+G+LHSD+D G+G KY+L+GEGAGT+FVID
 Sbjct: 45 GQVLQRSKRGWVNQFFVIEEYTGDPVLVGRHLSDSDGDNKIKYILSGEGAGTIFVID 104

Query: 463 EATGNIHVTKSLDREERAKQYVLLAQAVDRASNRPLEPSEFIIKQDINDNPPIFPLGPY 642
 + +GNIH TK+LDREE+AQY L+AQAVDR +NRLEPSEFI+K QDINDNPP F Y
 Sbjct: 105 DKSGNIHATKTLDREERAQYTLMAQAVDRDTRNRPSEFIVKQVQDINDNPPFEFLHETY 164

Query: 643 HATVPEMSNVGTSVIQVTAHDADDPYSGNSAKLVYTVLDGLPFFSVDPQTGVVVRTAIPNM 822
 HA VPE SNVGTSVIQTADDDP+YGNLSAKLVY++L+G P+FSV+ QTG++RTA+PNM
 Sbjct: 165 HANVPERSNVGTSVIQVTAHDADDPYSGNSAKLVYSILEGQPYFSVEAQTGIIRTAIPNM 224

Query: 823 DRETQEEFLVVIQAKDMGGMGGLSGSTTVTTLSDVNDNPPKFPQSLYQFSVVEAGPG 1002
 DRE +EE+ VVIQAKDMGGMGGLSG+T VT+TL+DVNDNPPKFPQS+YQ SV E A PG
 Sbjct: 225 DREAKEYHVVIQAKDMGGMGGLSGTKVTITLTDVNDNPPKFPQSVYQISVSEAAVPG 284

Query: 1003 TLVGRRLAQDQDPLGDNALMAYSILDGSEAFSISTDLQGRDGLLTVRKPLDFESORSYS 1182
 VGR++A+DPD+G+N L+ Y+I+DG+G E+F I+TD + ++G++ ++KP+DFE++R+YS
 Sbjct: 285 EEVGRVKAKDPDIDGENGLVTYNIVDGDMESFEITTDYETQEGVIKPKPVDFTKRAYS 344

Query: 1183 FRVEATNTLIDPAYLRGPFKDVASVRVAVQDAPEPPAFTQAAHYHLTVPENKAPGTLVGQ 1362
 +VEA N IDP ++ GPFKD +V++AV+DA EPP F +Y V EN A GT+VG+
 Sbjct: 345 LKVEAANVHIDPKFISNGPFKDTVTVKIAVEDADEPPMFLAPSYIHEVQENAAAGTVVGR 404

Query: 1363 ISAADLDSPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARAWNHLTVLATEL 1539
 + A D D+ SPIRYSI H+D +R +F+I PE+G I T PLDRE AW N+TV A E+
 Sbjct: 405 VHAKDPDAANSPIRYSIDRHTDLDRFFTNPEDGFIKTKPLDREETAWNLNITVFAAEI 463

FIG. 1

**BLASTX ALIGNMENT OF SEQ ID NO: 4, CADHERIN-LIKE POLYPEPTIDE WITH HUMAN
SEQUENCE ENCODED BY HUMAN OSF-4-1 cDNA POLYPEPTIDE SEQ ID NO: 17**

Query: Cadherin-like plypeptide (SEQ ID NO: 4)
 Subjct: sp|R49731|R49731 Sequence encoded by human OSF-4-1 Cdna (SEQ ID NO: 17)
 Length = 796

Score = 1478 (525.3 bits), Expect = 1.2e-164, Sum P(2) = 1.2e-164
 Identities = 269/419 (64%), Positives = 341/419 (81%), Frame = +1

Query:	283	GPALLRRSWVNQFFVIEEYAGPEPVLIGKLHSDVDRGEGRTKYLTTGEGAGTVFVID	462
Sbjct:		G L R++R WVNQFFVIEEY GP+PVL+G+LHSD+D G+G KY+L+GEGAGT+FVID	
	45	GQVLQSKRGWVNQFFVIEEYTGPDPLVGLRLHSDIDSDGDNIKYILSGEGAGTIFVID	104
Query:	463	EATGNIHVTKSLDREEKAQYVLLAQAVDRASNRPLEPSEFIIKQDINDNPPIFPLGPY	642
Sbjct:		+ +GNIH TK+LDREE+AQY L+AQAVDR +NRLEPSEFI+K QDINDNPP F Y	
	105	DKSGNIHATKTLDRERAQYTLMAQAVDRDTRNRPSEFIVKVQDINDNPPEFLHETY	164
Query:	643	HATVPEMSNVGTSVIOVTAHDADDPSYNSAKLVYTVLDGLPFFSVDPQTGVVVRTAIPNM	822
Sbjct:		HA VPE SNVGTSVIOVTA DADDP+YGNsAKLVY++L+G P+FSV+ QTG++RTA+PNM	
	165	HANVPERSNVGTSVIOVTASDADDPYGNsAKLVYSILEGQPYFSVEAQTGIIRTALENM	224
Query:	823	DRETQEEFLVVIQAKDMGGMGGLSGSTVTVTLSVDNDNPPKFPQSLYQFSVVETAGPG	1002
Sbjct:		DRE +EE+ VVIQAKDMGGMGGLSG-T VT+TL+DVNDNPPKFPQS+YQ SV E A PG	
	225	DREAKEYHVVIQAKDMGGMGGLSGTKVTITLTDVNDNPPKFPQSVYQISVSEAAVPG	284
Query:	1003	TLVGRLRAQDPDLGDNALMAYSILDGEGSEAFSISTDLQGRDGLLTVRKPLDFESQRSYS	1182
Sbjct:		VGR++A+DPD+G+N L+ Y+I+DG+G E+F I+TD + ++G++ ++KP+DFE++R+YS	
	285	EEVGRVKAQDPDIDGGLVNTYNIVDGGMESFEITTDYETQEGVIKPKPVDFTKRAYS	344
Query:	1183	FRVEATNTLIDPAYLRGPFKDVASVRVAVQDAPEPAFTQAAHYHLTVPENKAPGTLVGQ	1362
Sbjct:		+VEA N IDP ++ GPFKD +V++AV+DA EPP F +Y V EN A GT+VG+	
	345	LKVEAANVHIDPKFISNGPFKDTVTVKIAVEDADEPPMFLAPSYIHEVQENAAAAGTVVGR	404
Query:	1363	ISAADLSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARAWNLTVLATEL	1539
Sbjct:		+ A D+ SPIRYSI H+D +R F+I PE+G I T PLDRE AW N+TV A E+	
	405	VHAKDPDAANSPIRYSIDRHTDLDRFTINPEDGFIKTKPLDREETAWLNITVFAAEI	463

FIG. 2